Amendments to the Claims:

This listing of claims will replace all prior versions and listings of claims in the application:

LISTING OF CLAIMS

1. *(**currently** amended):* A method for determining the presence or absence of at least one target sequence (2) in a nucleic acid sample, comprising the steps of:

a) providing to a nucleic acid sample a pair of a first oligonucleotide probe and a second oligonucleotide probe for each target sequence to be detected in the sample, whereby the first oligonucleotide probe has a section (4) at its 5'-end that is complementary to a first part (5) of a target sequence and the second oligonucleotide probe has a section (6) at its 3'-end that is complementary to a second part (7) of the target sequence,

wherein ~~whereby~~ the first (5) and second part (7) of the target sequence are located adjacent to each other, and

wherein ~~whereby~~ the first and second oligonucleotide probes (4, 6) each comprise a tag sequence (8, 9), which ~~whereby the~~ tag sequences

(i) are essentially non-complementary to the target sequence, ~~whereby the tag sequences~~

(ii) comprise primer-binding ~~sequences~~ sites (12, 13), and

wherein at least one of the tags further comprises a stuffer (11) and a restriction site (10) for a restriction enzyme,

(A) which restriction site (10) is located between the primer-binding site and the section of the oligonucleotide probe (4, 6) that is complementary to the first (5) or second part (7) of the target sequence and ~~wherein the~~

(B) which stuffer (11) is located between the restriction site (10) and the primer-binding site;

b) allowing the oligonucleotide probes to anneal to the adjacent parts of target sequence so that ~~whereby~~ the complementary sections (4,6) of the first and the second oligonucleotide probes are adjacent;

c) providing means (14) for connecting the first and the second oligonucleotide probes annealed adjacently to the target sequence and allowing the complementary sections (4, 6) of the adjacently annealed first and second oligonucleotide probes to become connected, to produce a connected probe (15) corresponding to a target sequence in the sample;

d) amplifying the connected probes from a primer pair (16, 17) to produce an amplified sample (19) comprising amplified connected probes (20);

e) digesting the amplified connected probes with the restriction enzyme to produce a detectable fragment (21);

f) detecting the presence or absence of the target sequence by detecting the presence or absence of the detectable fragment by a detection method based upon molecular mass.

2. ***(currently amended):*** A method according to claim 2, wherein the mass of a detectable fragment corresponding to a target sequence in a sample differs ~~in mass~~ from the mass of a detectable fragment corresponding to a different target sequence in the sample.

3. ***(currently amended):*** A method according to claim 2 [[or 3]], wherein the detectable fragment is denatured to provide a top single strand and a bottom single strand.

4. ***(currently amended):*** A method according to claim 3, wherein the top strand ~~is a single stranded oligonucleotide comprising~~ comprises the stuffer and wherein the bottom strand is essentially complementary to the top strand.

5. ***(currently amended):*** A method according to claim 3[[-4]], wherein the mass of a top strand corresponding to one [[a]] target sequence in a sample differs from the [[in]] mass of ~~from~~ the top strand corresponding to a different target sequence in the sample.

6. ***(currently amended):*** A method according to claim 3[[-4]], wherein the mass of a bottom strand corresponding to one [[a]] target sequence in a sample differs from the [[in]] mass of ~~from~~ the bottom strand corresponding to a different target sequence in the sample.

7. ***(currently amended):*** A method according to claim 3 [[2-5]], wherein the difference in mass is due to ~~provided by~~ the mass of the stuffer in the top strand.

8. ***(currently amended):*** A method according to ~~any one of claims~~ claim 3 [[-7]], wherein the top strands and/or the bottom strands corresponding to different target sequences in the sample differ in mass by more than 1 Dalton.

9. ***(currently amended):*** A method according to ~~claims~~ claim 1[[-8]], wherein a primer capable of annealing to the primer-binding site in the detectable fragment comprises an affinity label.

10. ***(currently amended):*** A method according to claim 9, wherein the top strands and/or the bottom strands comprise the affinity label.

11. *(currently amended):* A method according to claim 9 [[or 10]], wherein the detectable fragment, the top strand or the bottom strand is purified or ~~/~~isolated~~/~~ or separated from the sample comprising the amplified connected probes using the affinity label.

12. *(currently amended):* A method according to claim 9[[-11]], wherein the affinity label is biotin.

13. *(currently amended):* A method according to ~~claims~~ claim 1[[-12]], wherein the detection method is a ~~based on~~ mass spectroscopic~~spectrometry~~ method~~, such as HPLC-MS, GC-MS, MALDI-TOF, ESI-MS~~.

14. *(currently amended):* A method according to ~~claims~~ claim 1[[-13]], wherein the restriction enzyme is a restriction endonuclease.

15. *(currently amended):* A method according to claim 14[[15]], wherein the restriction endonuclease is a rare cutter.

16. *(currently amended):* A method according to claim 3~~claims 1-15~~, wherein a further ~~mass~~ difference in mass between top strands corresponding to different target sequences is created ~~provided~~ by incorporating different primer-binding sites in the oligonucleotide probes to which the different primers can anneal~~, preferably with a similar priming efficiency~~.

17. *(currently amended):* A method according to ~~any one of the preceding claims~~ claim 1, wherein the tag of the oligonucleotide probes comprise [[a]] said stuffer sequence with a mass from 0 to 20,000 daltons~~, preferably from 100 to 10000, more preferably from 500 to 5000~~.

18. *(currently amended):* A method according to claim 1~~any one of the preceding claims~~, wherein the presence or absence of at least 10~~, , preferably at least 25, more preferably at least 50, still more preferably at least 100, most preferably at least 250~~ different target nucleotide sequences is determined in a nucleic acid sample.

19. *(currently amended):* A method according to claim 1~~any one of the preceding claims~~, wherein the length of the complementary section of the oligonucleotide probes is between 15 and 50 nucleotides.

20. *(currently amended):* A method according to ~~any one of the preceding claims~~claim 1, wherein the length of the primer-binding site is between 12 and 40 nucleotides~~, preferably between 15 and 30 nucleotides, more preferably between 17 and 25~~.

21. *(**currently** amended):* A method according to ~~any one of the preceding claims~~claim 1, wherein the length of the tag is between 15 and 540 nucleotides~~, preferably between 18 and 140 nucleotides, more preferably between 20 and 75~~.

22. *(**currently** amended):* A method according to ~~any one of the preceding claims~~claim 1, wherein the target nucleotide sequence contains a polymorphism~~, preferably a single nucleotide polymorphism~~.

23. *(**currently** amended):* A method according to ~~any one of the preceding claims~~claim 1, wherein the target nucleotide sequence is ~~a DNA molecule selected from the group consisting of:~~ cDNA, genomic DNA, a restriction fragment[[s]], an adapter-ligated restriction fragment[[s]], amplified adapter-ligated restriction fragments or ~~and~~ AFLP fragments.

24. *(**currently** amended):* A method according to ~~any one of the preceding claims~~claim 1, further comprising a step for ~~the removal of~~ removing non-ligated probes~~, optionally prior to amplification, preferably by exonucleases~~.

25. *(**currently** amended):* A method according to claim 1~~any of the preceding claims~~, wherein at least one of the primers is a selective primer.

26. *(**currently** amended):* A method according to claim 25, wherein the selective primer comprises

(i) a section that is complementary to at least part of the primer-binding site, and

(ii) ~~further contains~~ a selective section of one to 10 selective nucleotides~~, preferably~~ located immediately adjacent, to the 3' end of the section of (i)~~complementary to the primer binding site~~.

27. *(**currently** amended):* A method according to claim ~~25 or~~ 26 wherein the section of (i) ~~that is complementary to at least part of the primer binding site preferably~~ is complementary to 5~~, 10, 11, 12, 12, 14, 15, 16~~ or more nucleotides that form a part of the primer-binding site ~~sequence~~ that is located immediately adjacent~~, preferably at the 5'end,~~ to the nucleotides complementary to the selective section of the primer.

28-32: CANCEL

33. *(withdrawn; currently amended):* A oligonucleotide acid probe for use in a method according to claim 1~~as defined in claims 1-27.~~

34. *(withdrawn; currently amended):* A set of two or more oligonucleotide probes, for use in a method according to claim 1~~as defined in claims 1-27~~.

35. CANCEL

36. *(withdrawn; currently amended):* A set of primers for use in a method according to claim 1 ~~any one of claims 1-27.~~

37. *(withdrawn; currently amended):* A kit comprising oligonucleotide probes suitable for use in a method according to claim 1~~as defined in claims 1-27~~.

38. *(withdrawn; currently amended):* A kit comprising primers for use in a method according to claim 1~~as defined in claims 1-27~~.

39. *(withdrawn; currently amended):* A kit according to claim 38 further comprising ~~primers and~~ oligonucleotide probes ~~for use in a method as defined in claims 1-27~~.